

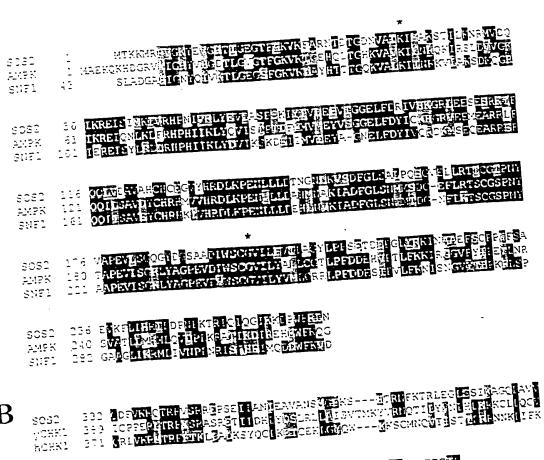
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Kinase Regulatory Domain

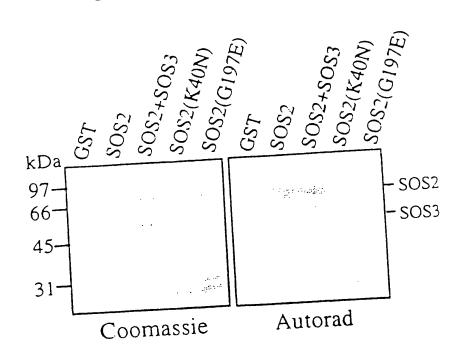
TOGATCAGATAAAAGTTTG<u>TAA</u>AGA B ATGACAMAGAMATGAGAAGAGTGGGCMAGTAGGAGGTTGGTGGCACAATAGGTGAAGGMCTTTTGCTAAGGTTAAG * M T K K M R R V G K Y E V G R T T T T A K K THTSCSAGGAACACAGACACTGGTGATAATGTAGCCATCALLATTATSGCTALGAGTACALTACTTALGAACAGAATG GTTSATCAGATAAAAAGAGAGATATCTATAATGAAGATTGTTCGTCACCSSAACATAGTSAGGTGTATGAGGTGTTG 53 V D Q I X R I III -GCGAGTCETTCGAAAATATATATATAGTTTGGAGTTTGGACAGGAGAGAGTCTTTGATAGAATTGTTCATAAAGGG 79 A S P S K I Y I V L E F V T 3 G E L F 3 R I V H K S AGGCTTGAAGAAAATTGAGTCTCGGAAATACTTTCAACAGCTTGTAGATGCTGTTGCTCATTGTCACTGCAAGGGTGTT AGGCTTGAAGANAGTGAGTCTCGGAAATACTTTCAACAGCTTGTAGATUC.STAGAT TACCACCOTGACCTALAGCCLGLALATCTTTACTCGATACALATGGALATCTGAAGGTTTCSGATTTCGGACTCAGT 131 Y R Y K P S E L D T N G N E K Y S VII --GCATTGCCTCAGGAAGGAGTAGAACTTCT3CGTACCACATGTSGAACTCCGAACTATGTAGTTCTAGAGGGTACTTAGT GCATTGCCTCAGGAAGAACTAGAACTTCTGCGTACCACATGTGGAACTCTAGAACTACAACTTTGGAACTCACATGTGGAACTCTAGAACTTCTGCGTACCACATGTGGAACTCTAGAACTAGAACAACTAGAACAACAACAACAACAACAACAACAACAACAA GGACAGGGTTACSATGGTTCAGCAGCTSATATTTSGTCTTGCGGGGGTTATTCTTTACGTTATATTGGCTGGATATTTA CCTTTTCCGAGACGGATCTTCCAGGGTT.STACAGAAAAATAAATGCAGCAGAGATTTCTTGCACCGTGGTTTTCCC 209 P F S E T D L ? G L Y R K I N A A E F S C ? ? W F S GCAGAAGTGAAGTTTTTAATACATAGGATACTTGACCCCAATCCCAAACACGTATTCAAATTCAAGGAATCAAGAAA 235 A E V K F L I H R 1 L D P N P K T R I Q Q G I K X GATCCTTSGTTCAGATTAAATTATGTGCCTATACGAGCAAGGAAGAAGAAGAAGAAGAAGTAATTTGGATGATATTCGTGCA 261 D P W F R L N Y V P I R A R E Z E E V N L D D I R A 287 V F D G I E G S Y V A E N V E R N D E G P L M M N A TTTGAGATGATTACCTTATCACAAGGCTTAAATTTATCTGCACTATTTGACAGGCGACAGGATTTAAAAGGCCAA 313 F S M I T L S Q G L N L S A L ? D 3 R Q D F V K R Q ACCCGTTTTGTTTCTCGAAGGGAACCTAGTGAGATAATTGCTAACATTGAGGCTGTAGCGAACTCAATGGGTTTTAAG 339 T R P V S R R E P S E I I A N I E A V A N S M G F K TCTCATACACGAAACTTCAAGACAAGGCTCGAGGGATTATCTTCGATCAAGGCCGGACAGTTAGCTGTTGTGATAGAG 365 S H T R N F K T R L E G L S S I K A G Q L A V V I E 391 I Y E V A P S I F M V D V R K A A G E T L E Y H K P TACAAGAAGCTATGTTCGAAACTGGAAAACATAATATGGAGGGCAACAGAAGGAATACCAAAGTCAGAGATTCTCAGA 417 Y K K L C S X L E N I I H R A T E G I P K S E 1 L R ACAATCACGTTTTGATCCCAACTTAA

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